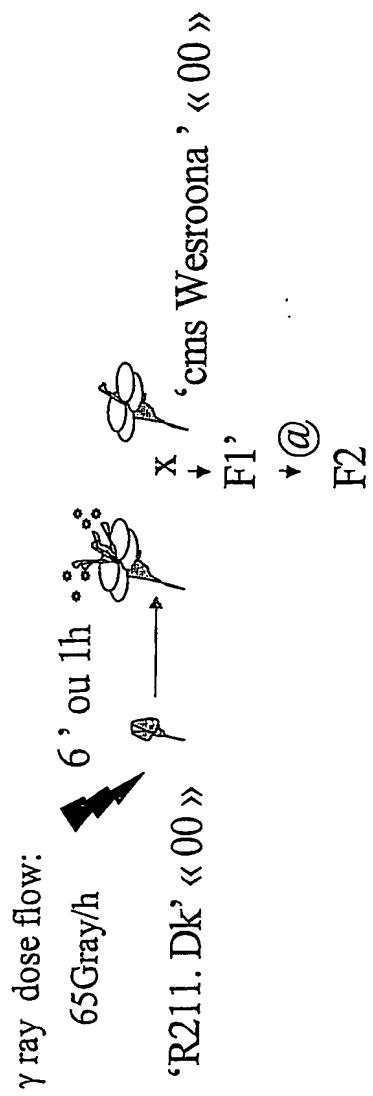


Fig 1



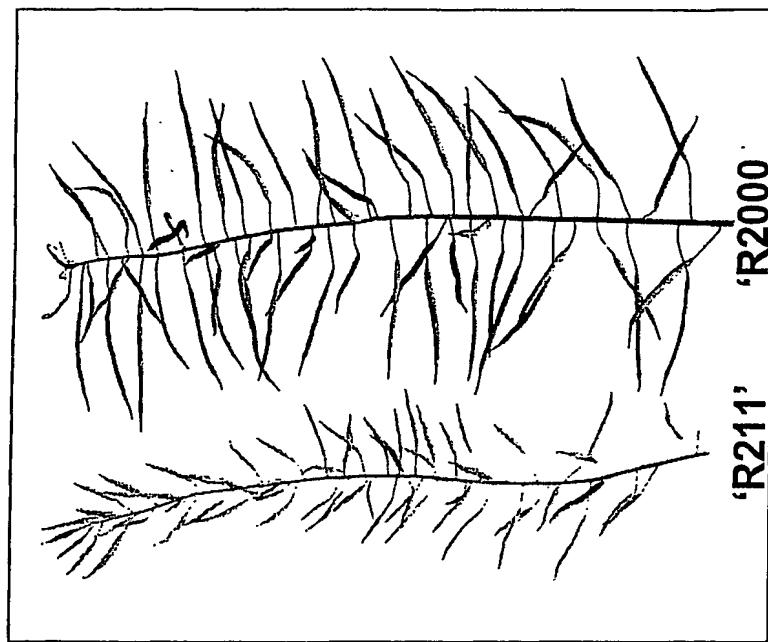


Fig. 1: Seed set on 'R211' and 'R2000'

Fig 2

Genotype	Selfings	Test Crosses
Drakkar	29.3	
Pactol	23.1	
R211	11.2	25.5
R2000	26.5 (24.0 – 31.1)	27.0 (24.0 – 28.7)

Fig 3

Fig 4

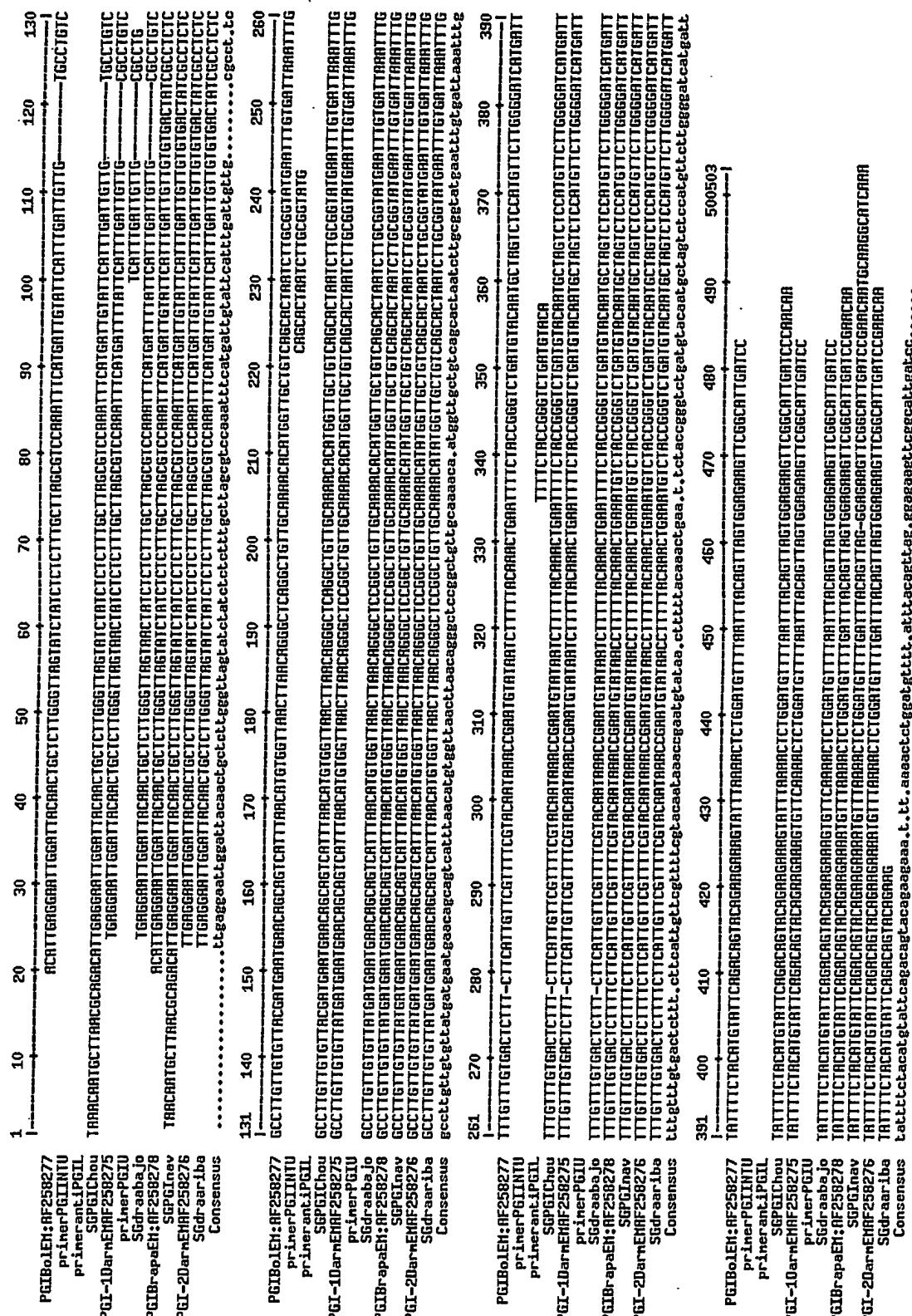


Fig 5

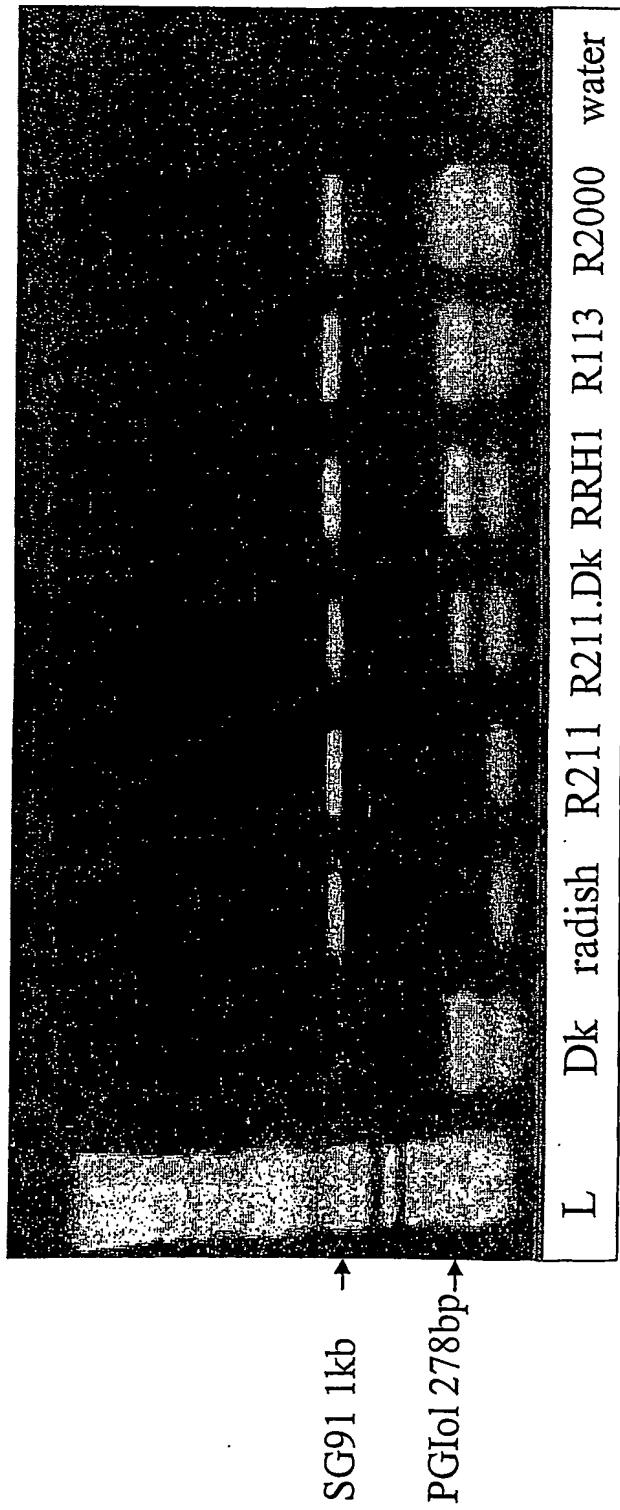
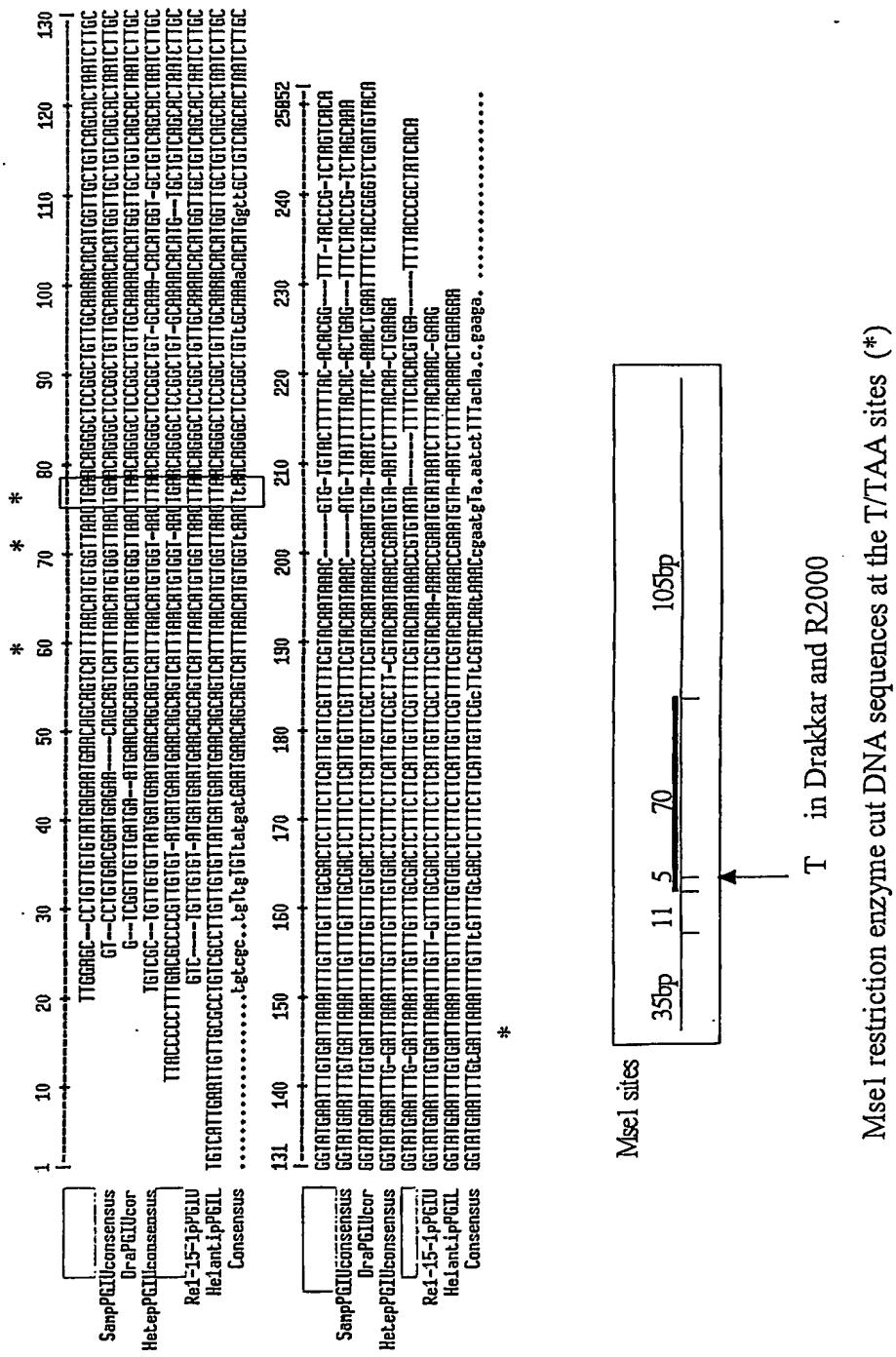


Fig 6



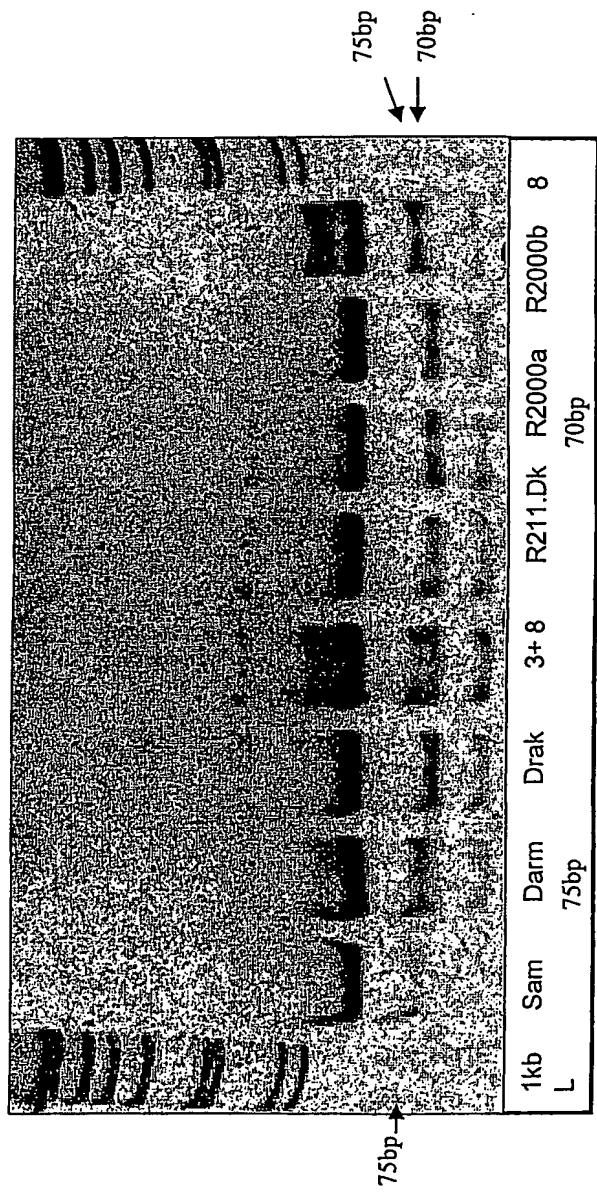
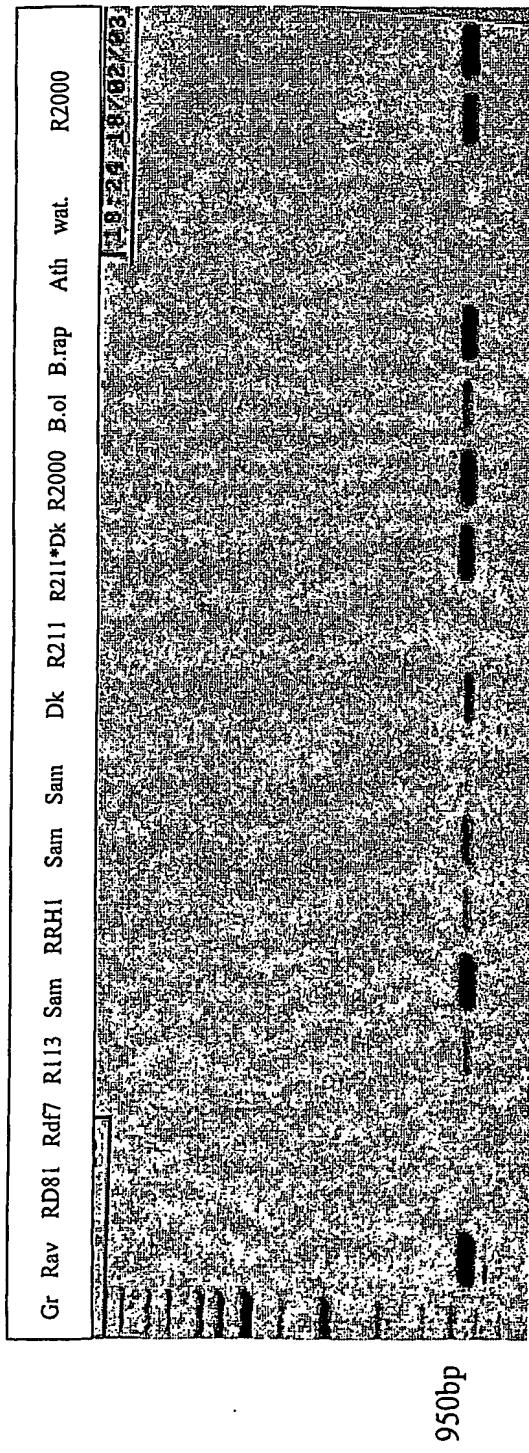


Fig 7

REQUEST AVAILABLE COPY

Fig 8



950bp

Fig 9

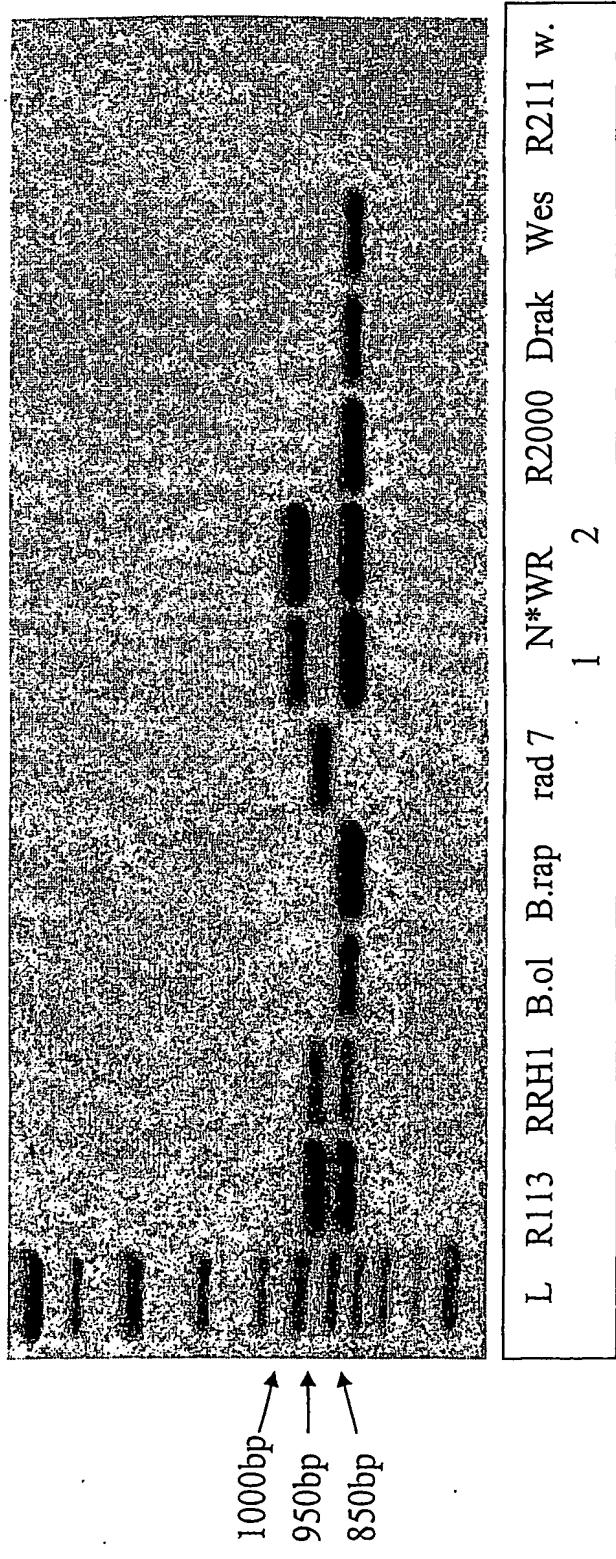
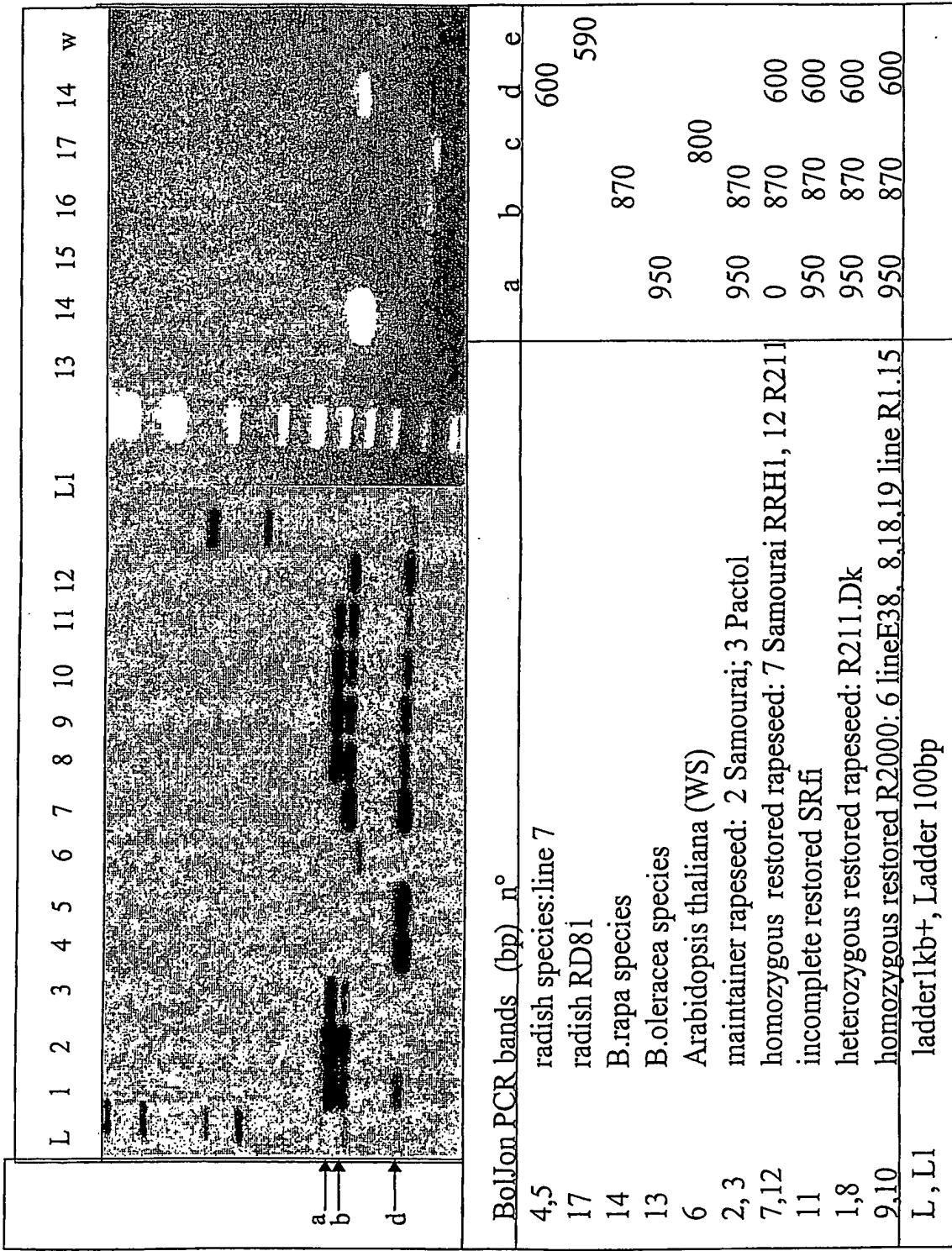


Fig 10



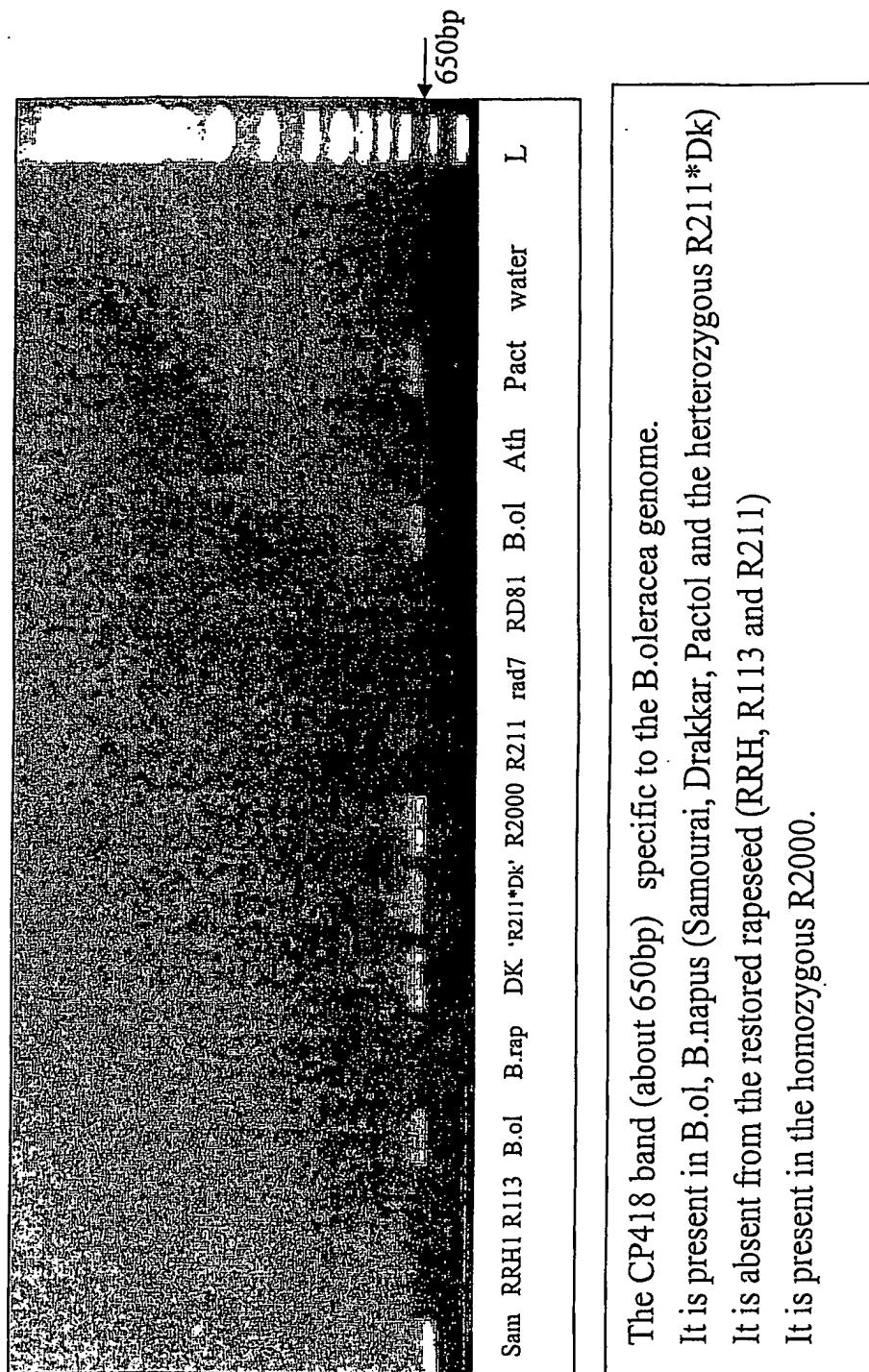


Fig 11

The CP418 band (about 650bp) specific to the *B.oleracea* genome.
It is present in *B.ol*, *B.napus* (*Samourai*, *Drakkar*, *Pactol* and the heterozygous *R211*Dk*)
It is absent from the restored rapeseed (*RRH*, *R113* and *R211*)
It is present in the homozygous *R2000*.

Figure 12

Figure 13 (a)

consePGIintTUNDrakka	51	81 PGInt U -->	100
consensWesrPGI			
consePGIintUNTR113			
consePGIintUNTBrapaA			
ConsePGIintUNTRRH1			
PGIBo-EM:AF258277	TTGCTTAGCG	TCCAAATTTC ATGATTGTAT	TCATTGATT GTTGTG...
PGIBra-EM:AF258278	TTGCTTAGCG	TCCAAATTTC ATGATTGTAT	TCATTGATT GTTGTGTGAC
consePGIintUNTBolera			
consePGIintUNTR2000		TTG...	TCATT.GA... TTGT.TGCG
Consensus			1
consePGIintTUNDrakka	101	-->	150
consensWesrPGI			
consePGIintUNTR113			
consePGIintUNTBrapaA			
ConsePGIintUNTRRH1			
PGIBo-EM:AF258277	CCTG	TCGCCTGTTG TGTTA.GATG AAT.GAACAG CAGTCATTAA	
PGIBra-EM:AF258278	TATCGCCTC.	TCGCCTGTTG TGTTATGATG AAT.GAACAG CAGTCATTAA	
consePGIintUNTBolera			
consePGIintUNTR2000			
Consensus	CCTG	TCGCCTGTTG TGTTATGATG AAT.GAACAA CAGTCATTAA	cagtcattta
consePGIintTUNDrakka	151	* MseI restriction site	200
consensWesrPGI	ACATG.TGGT	TAACTAAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG	
consePGIintUNTR113	ACATG.TGGT	TAACTAAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG	
consePGIintUNTBrapaA	ACATG.TGGT	.AACTGAACA GGGCTCCGGC TGTTGCC.. CTAAGGGTTG	
ConsePGIintUNTRRH1	ACATGGTGGT	TAACTGAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG	
PGIBo-EM:AF258277	ACATG..GGT	..ACTGAACA GGGC.CCGGC TGTTGCAA.. ACAG..TG	
PGIBra-EM:AF258278	ACATG.TGGT	TAACTAAACA GGGCTCAGGC TGTTGCAAAA CACATGGTTG	
consePGIintUNTBolera	ACATG.TGGT	TAACTAAACA GGGCTCCGGC TGTTGCAAAA CATATGGTTG	
consePGIintUNTR2000	C TGTTGCAAAA CACATGGTTG	
Consensus	ACATG.TGGT	TAACTAAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG	cacatggttg
consePGIintTUNDrakka	201	PGI int U -->	250
consensWesrPGI	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTGTTGTTGTT
consePGIintUNTR113	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTGTTGTTGTT
consePGIintUNTBrapaA	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTGTTGTTGTT
ConsePGIintUNTRRH1	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTGTTGTTGTT
PGIBo-EM:AF258277	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTGTTGTTGTT
PGIBra-EM:AF258278	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTGTTGTTGTT
consePGIintUNTBolera	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTGTTGTTGTT
consePGIintUNTR2000	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTGTTGTTGTT
Consensus	ctgtcagcac	taatcttgc ggtatg	aatt tgtgattaaa ttgttgtt
consePGIintTUNDrakka	251		300
consensWesrPGI	TGTGACTCTT	T.CTTCATTG TTGCTTTTCG TACAATAAAC CGAATGTATA	
consePGIintUNTR113	TGTGACTCTT	T.CTTCATTG TTGCTTTTCG TACAATAAAC CGAATGTATA	
consePGIintUNTBrapaA	TGCGACTCTT	T.CTTCATTG TTGCTTTTCG TACAATAAAC ..AATGTATA	
ConsePGIintUNTRRH1	TGCGACTCTT	T.CTTCATTG TTGCTTTTCG TACAATAAAC ..AATGTATA	
PGIBo-EM:AF258277	TGTGACTCTT	T.CTTCATTG TTGCTTTTCG TACAATAAAC CGAATGTATA	
PGIBra-EM:AF258278	TGTGACTCTT	TTCTCATTG TTGCTTTTCG TACAATAAAC CGAATGTATA	
consePGIintUNTBolera	TG.GACTCTT	T.CTTCATTG TTGCTTTTCG TACAATAAAC CGAATGTATA	
consePGIintUNTR2000	TGTGACTCTT	T.CTTCATTG TTGCTTTTCG TACAATAAAC CGAATGTATA	
Consensus	tg.gactctt	t.cttcattg ttgctttcg tacaataaac	cgaaatgtata

Figure 13 (b)

	301	<--- PGIol antL 341 --->	350
consePGIintTUNDrakka	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consensWesrPGI	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consePGIintUNTR113	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consePGIintUNTBrapaA	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
ConsePGIintUNTRRH1	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
PGIBo-EM:AF258277	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
PGIBra-EM:AF258278	ACCTTTTAC AAACTGAA	AT GTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consePGIintUNTBolera	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consePGIintUNTR2000	ATCTTT.AC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
Consensus	atcttttac aaactgaa	tt ttctaccggg tctgatgtac a atgctAGTC	

Figure 14 (a)

201	PGI int U --->	250
consePGIintTUNDrakka	CTGT CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGT
consensWesrPGI	CTGT CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGT
consePGIintUNTR113	CTGT CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGT
consePGIintUNTBrapaA	CTGT CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGT
ConsePGIintUNTRRH1	CTGT CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGT
PGIBo-EM:AF258277	CTGT CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGT
PGIBra-EM:AF258278	CTGT CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGT
consePGIintUNTBoleta	CTGT CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGT
consePGIintUNTR2000	CTGT CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGT
Consensus	ctgtcagcac taatcttgc ggtatg	aatt tgtgattaaa tttgtttgt
 251		
consePGIintTUNDrakka	TGTGACTCTT T.CTTCATCG TTCGTTTCG TACAATAAAC	CGAATGTATA
consensWesrPGI	TGTGACTCTT T.CTTCATCG TTCGTTTCG TACAATAAAC	CGAATGTATA
consePGIintUNTR113	TGCGACTCTT T.CTTCATCG TTCGTTTCG TACAATAAAC	..AATGTATA
consePGIintUNTBrapaA	TGCGACTCTT T.CTTCATCG TTCGTTTCG TACAATAAAC	..AATGTATA
ConsePGIintUNTRRH1	TGCGACTCTT T.CTTCATCG TTCGTTTCG TACAATAAAC	..AATGTATA
PGIBo-EM:AF258277	TGTGACTCTT T.CTTCATCG TTCGTTTCG TACAATAAAC	CGAATGTATA
PGIBra-EM:AF258278	TGTGACTCTT TTCCTCATCG TTCGTTTCG TACAATAAAC	CGAATGTATA
consePGIintUNTBoleta	TG.GACTCTT T.CTTCATCG TTCGTTTCG TACAATAAAC	CGAATGTATA
consePGIintUNTR2000	TGTGACTCTT T.CTTCATCG TTCGTTTCG TACAATAAAC	CGAATGTATA
Consensus	tg.gactctt t_citccatcg ttccgtttcg tacaataaac	cgaaatgtata
e		
301 <--- PGIol antL 341 350		
consePGIintTUNDrakka	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
consensWesrPGI	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
consePGIintUNTR113	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
consePGIintUNTBrapaA	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
ConsePGIintUNTRRH1	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
PGIBo-EM:AF258277	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
PGIBra-EM:AF258278	ACCTTTTAC AAACTGAA	AT GTCTACCGGG TCTGATGTAC A ATGCTAGTC
consePGIintUNTBoleta	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
consePGIintUNTR2000	ATCTTT.AC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
Consensus	atcttttac aaactgaa	tt ttctacccggg tctgatgtac a atgctAGTC
e		
351 400		
consePGIintTUNDrakka	TCCATGTTCT TGGGGATCAT GATTATTTT CTACATGTAT	TCAGACAGTA
consensWesrPGI	TCCATGTTCT TGGGGATCAT GATTATTTT CT.CATGTAT	TCAGACAGTA
consePGIintUNTR113	TCCATGTTCT TGGGGATCAT GATTATTTT CTACATGTGT	TCAGCCAGTA
consePGIintUNTBrapaA	TCCATGTTCT TGGGGATCAT GATTATTTT CTACATGTGT	TCAGCCAGTA
ConsePGIintUNTRRH1	TCCATGTTCT TGGGGATCAT GATTATTTT CTACATGTGT	TCAGCCAGTA
PGIBo-EM:AF258277	TCCATGTTCT TGGGGATCAT GATTATTTT CTACATGTAT	TCAGACAGTA
PGIBra-EM:AF258278	TCCATGTTCT TGGGGATCAT GATTATTTT CTACATGTAT	TCAGACAGTA
consePGIintUNTBoleta	TCCATGTTCT TGGGGATCAT GATTATTTT CTACATGTAT	TCAGACAGTA
consePGIintUNTR2000	TCCATGTTCT TGGGGATCAT GATTATTTT CTACATGTAT	TCAGACAGTA
Consensus	TCCATGTTCT TGGGGATCAT GATTATTTT CTaCATGTAT	TCAGACAGTA
e 5 e 6		
401 450		
consePGIintTUNDrakka	CAGAAGAAAG TGTT AAAAC TCTGGATGTT TTAATTTACA	GTTAGTGGAG
consensWesrPGI	CAGAAGAAAG TGTT AAAAC TCTGGATGTT TTAATTTACA	GTTAGTGGAG
consePGIintUNTR113	CAGAAGAAAG TGTTAAAAC TCTGGATGTT TTAATTTACA	GTTAGTGGAG
consePGIintUNTBrapaA	CAGAAGAAAG TGTTAAAAC TCTGGATGTT TTAATTTACA	GTTAGTGGAG
ConsePGIintUNTRRH1	CAGAAGAAAG TGTTAAAAC TCTGGATGTT TTAATTTACA	GTTAGTGGAG
PGIBo-EM:AF258277	CAGAAGAAAG TATTTAAAAC TCTGGATGTT TTAATTTACA	GTTAGTGGAG
PGIBra-EM:AF258278	CAGAAGAAAA TGTTAAAAC TCTGGATGTT TTGATTTACA	GTTAGTGGAG
consePGIintUNTBoleta	CAGAAGAAAG TGTT AAAAC TCTGGATGTT TTAATTTACA	GTTAGTGGAG
consePGIintUNTR2000	CAGAAGAAAG TGTT AAAAC TCTGGATGTT TTAATTTACA	GTTAGTGGAG
Consensus	CAGAAGAAAa TgTT AAAAC TCTGGATGTT TTaATTTACA	GTTAGTGGAG
e 7 e		

Figure 14 (b)

Figure 14 (c)

	701	750
consePGIintTUNDrakka consensWesrPGI consePGIintUNTR113 consePGIintUNTBrapaA ConsePGIintUNTRRH1 PGIBo-EM:AF258277 PGIBra-EM:AF258278 consePGIintUNTBolera consePGIintUNTR2000 Consensus	CATATTCTTT CTATTTTATT TTCCCTCTAA TGATTTCTTC TTTTTTTAT CATATTCTTT CTATTTTATT TTCCCTCTAA TGATTTCTTC TTTTTTTAT CATATTCTTT CTATTTTATT TTCCCTCTGAA TGATTTCTTC TCTTTTAT.. CATATTCTTT CTATTTTATT TTCCCTCTGAA TGATTTCTTC TCTTTTAT.. CATATTCTTT CTATTTTATT TTCCCTCTGAA TGATTTCTTC TCTTTTAT.. CATATTCTTT CTATTTTATT TTCCCTCTAA TGATTTCTTC TTTTTTTA.. CATATTCTTT CTATTTTATT TTCCCTCTAA TGATTTCTTC TTTTTTTAT catattcttt ctatttatt ttccctt.aa tgatttcttc ttttt.t...	15 16 17
	751	800
consePGIintTUNDrakka consensWesrPGI consePGIintUNTR113 consePGIintUNTBrapaA ConsePGIintUNTRRH1 PGIBo-EM:AF258277 PGIBra-EM:AF258278 consePGIintUNTBolera consePGIintUNTR2000 Consensus	TGCATTCCCG TTTTATTTTC AAAAGTTGTT ACTGTCTCTA AATCAAGAAG TGCATTCCCG TTTTATTTTC AAAAGTTGTT ACTGTCTCTA AATCAAGAAG TGCATTCCCG TTTTATTTTC AAAAGTTGTC ACTGTCTCTA AATCAAGAAG TGCATTCCCG TTTTATTTTC AAAAGTTGTC ACTGTCTCTA AATCAAGAAG TGCATTCCCG TTTTATTTTC AAAAGTTGTC ACTGTCTCTA AATCAAGAAG TGCATTCCCG TTTTATTTTC AAAAGTTGTC CGGCCCCCTA AACCAAGAAG TGCATTCCCG TTTTATTTTC AAAAGTTGTT ACTGTCTCTA AATCAAGAAG tgcatccccg ttttattttc aaaagttgt. actgtctcta aatcaagaag	800
	801	850
consePGIintTUNDrakka consensWesrPGI consePGIintUNTR113 consePGIintUNTBrapaA ConsePGIintUNTRRH1 PGIBo-EM:AF258277 PGIBra-EM:AF258278 consePGIintUNTBolera consePGIintUNTR2000 Consensus	AAACCTTCTT AGTAGATCCA GGTGATATTG AGCCTTTTT AAATTGGACT AAACCTTCTT AGTAGATCCA GGTGATATTG AGCCTTTTT AAATTGGACT AAACCTTCTT AGTAGATCCA GTTGATATTG AGCCTTTCT AAATTGGACT AAACCTTCTT AGTAGATCCA G.TGATATTG AGCCTTTCT AAATTGGACT AAACCTTCTT AGTAGATCCA GTTGATATTG AGCCTTTCT AAATTGGACT AAACCTTCTT AGGA...CCA GA...CTCC ACCCTTTTT AAATTGGACT AAACCTTCTT AGTAGATCCA GGTGATATTG AGCCTTTTT AAATTGGACT aacaccttctt agtagatcca g.tgatattc agcctttt.aaattggact	18 19
	851	900
consePGIintTUNDrakka consensWesrPGI consePGIintUNTR113 consePGIintUNTBrapaA ConsePGIintUNTRRH1 PGIBo-EM:AF258277 PGIBra-EM:AF258278 consePGIintUNTBolera consePGIintUNTR2000 Consensus	GCAGGTTTTT AAA.GGGAGC TTCAAGCATT GATAAGCATT TCCAGTCCCC GCAGGTTTTT AAA.GGGAGC TTCAAGCATT GATAAGCATT TCCAGTCCAC GCAGGTTTTT AAA.GGGAGC TTCAAGCATT GATCAGCATT TCCAGTCC.. GCAGGTTTTT AAA.GGGAGC TTCAAGCATT GATCAGCATT TCCAGTCC.. GCAGGTTTTT AAA.GGGAGC TTCAAGCATT GATCAGCATT TCCAGTCCAC GCAGGTTTTT AAA.GGGGGC TTCAAGCATT GATAAGCATT TCCAGTCCAC GCAGGTTTTT AAACGGGAGC TTCAAGCATT GATAAGCATT TCCAGTCCAC gcaggttttt aaa.gggagc ttcaaggatt gat.agcatt tccagtcc.c	20
	901	950
consePGIintTUNDrakka consensWesrPGI consePGIintUNTR113 consePGIintUNTBrapaA ConsePGIintUNTRRH1 PGIBo-EM:AF258277 PGIBra-EM:AF258278 consePGIintUNTBolera consePGIintUNTR2000 Consensus	ACC.GTTTGAA GAAGAAATATA CCCGTGAGTT GCATTAGTT GTGTGATTAT ACC.GTTTGAA GAAGAAATATA CCCGTGAGTT GCATTAGTT GTGTGATTAT .CCCGTTGAA GAAGAAATATA CCCGTGAGTT GCATTAGTT ..GTGTGATTAT .CCCGTTGAA GAAGAAATATA CCCGTGAGTT GCATTAGTT GTGTGATTAT ACC.GTTTGAA GAAGAAATATA CCCGTGAGTT GCATTAGTT GTGTGATTAT ACCCGGTTGAA GAAGAAATATA CCCGTGAGTT GCATTAGTT GTGTGATTAT ACC.GTTTGAA GAAGAAATATA CCCGTGAGTT GCATTAGTT GTGTGATTAT acc.gtttga gaagaatata cccgtgagtt gcattagtt. gtgtgattat	950

Figure 14 (d)

	951	1000
consePGIinTUNDrakka	ACAGTTTTTC TTGTCTTTT GCTATGCCCA TCAACACTAG AAGATTG	GTG
consensWesrPGI	ACAGTTTT.C TTGTCTTTT. GCTATGTCCA TCAACACTAG A.GATTG	GTG
consePGIintUNTR113	ACAGTTTT.C TTGCCTTTTT GCTAT..AGG GCAAC.CTAG A.GATTCATG	
consePGIintUNTBrapaA	ACAGTTTT.C TTGTCTTTT. GCTATG.TCA TCAAC.CTAG A.GATTCATG	
ConsePGIintUNTRRH1	ACAGTTTT.C TTGTCTTTTT GCTAT...AT GCAACCCTAG ..GATTCATG	
PGIBo-EM:AF258277	
PGIBra-EM:AF258278	
consePGIintUNTBolera	ACAGTTTT.C TTGTCTTTTT GCTAG..TGA TCAAC.CTAG A.GATTG	GTG
consePGIintUNTR2000	ACAGTTTT.C TTGTCTTTTT GCTATGTCCA TCAACACTAG A.GATTG	GTG
Consensus	acagtttt.c ttgtctttt gctat....a tcaac.ctag a.gattc.tg	
	21	
	1001	1050
consePGIinTUNDrakka	AAGTTATTAG TGTAGCCAAC GCCTAGGGGG AGGTTGGTTG GCTGTTTGG	
consensWesrPGI	AAGTTATTAG TGTAGTCAAC GCA.....	
consePGIintUNTR113	AAGTTATTAG TGTAGTCAAC GCAGAGGAGA G..TTCACTG ACGG.....	
consePGIintUNTBrapaA	AAGTTATTAG TGTAGTCAAC GCAGAGTGAG AGG.TGATTG ..	
ConsePGIintUNTRRH1	AAGTTATTAG TGTAGTCAAC GCAGAGGGAG AGATGGTT..	
PGIBo-EM:AF258277	
PGIBra-EM:AF258278	
consePGIintUNTBolera	AAGTTATTAG TGTAGTCAAC GCATAGGGAG AGC.....	
consePGIintUNTR2000	AAGTTATTAG TGTAGTCAAC GCATAGGGAG AGGTGAT.GG TGACTTTGG	
Consensus	aagtatttag tgtagtcaac gca.agg.g. .g.....	
	1051	1076
consePGIinTUNDrakka	ACGTTTCAC GTGCTCCGGG GGGTTTTGG GGACCAAACC CCCAAC	
consensWesrPGI	
consePGIintUNTR113	
consePGIintUNTBrapaA	
ConsePGIintUNTRRH1	
PGIBo-EM:AF258277	
PGIBra-EM:AF258278	
consePGIintUNTBolera	
consePGIintUNTR2000	ACGATTCAG GTGCTTAGG GTTATTG ..	

Figure 15 (a)

<p>51</p> <pre> EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129bal-Drak GCPS18-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus </pre>	<p>100</p> <pre> CP418L AAACAAATCA AAATTCTAA TTTCTCCA AAAC TATGTA ACAAAAATCA AAATTGTAAA TGCTCCA AA CCAAAATCC AAATTGTAAA TGTTCCCT. CAAAATCCA AAATTGTAAA TGTC.CCT </pre>
<p>101</p> <pre> EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129bal-Drak GCPS18-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus </pre>	<p>150</p> <pre> AT A.CATTTCT GTAA AGG T.AT A.CATTTCT GTAA AGG TCAT A.CATTTCT GTAA TCACAAGGAC CTACAGAATA GAGTTATCAT AACATTT CT GTAA TCCTAACGAC TACAGAATA GAGTTATCAT AACATTTCT G AA TGGTAAACGGC CTCAAAAA.A GAGGTATCAA AAC.TTTCT GT.A TGGTTACCGC C.CAAAAA.A AAGGT..CAA AACTT.TCCG GTAA </pre>
<p>151</p> <pre> EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129bal-Drak GCPS18-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus </pre>	<p>200</p> <pre> TATTTCCAT CAAAATGA .. CTAGAGAAC AGCAGTCTT ATAACATTAT TATTTCCAT CAAAATGA .. CTAGAGAAC AG AGTTCIT ATAACATTAT ATATTTCCAT CAAAATGA .. CTAGAGAAC AG AGTTCIT ATAACATTAT ATATTTCCAT CAAAATGA .. CTAGAGAAC AG AGTTCIT ATAACATTAT ATGTTTCCAT CAAAATGA .. CTATCGAAC ATAATTAAT ATA.CATT ATGTTTCCAT CAAAATG .. CTATCGGAC ATAATTAAT ATAAC.TTCT ATGTTTCCAT CAAAATG .. CTTCGGA.C ATAATTAAT ATAAC.TTCT ATGTTTCCCT CAAA.TGG CTTCGGA.C ATAATTAAT A...CATTCT </pre>
<p>201</p> <pre> EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129bal-Drak GCPS18-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus </pre>	<p>250</p> <pre> CTGTAAA TG.TTCCAA CAAAA CCACT ACATAGCAGAGTTC .TTATAACAT CTGTAAA TG.TTCCAA CAAAA CCACT ACATAGCAGAGTTC ATTATAACAT CTGTAAA TG.TTCCAA CAAAA CCACT ACATAGCAGAGTTC .TTATAACAT CTGTAAA TG.TTCCAA CAAAA CCACT ACATAGCAGAGTTC .TTATAACAT CTG AAAATAATTCCCT CAAAAATTAA .. CATTC TTC TTACAA.A. CTG AAAAT ATTCCCT CAAAA TTAA ACATTC TTC T.AC AA.A. CTG AAA.TAAATTCCCT CAAAA TTAA ACATTC TTC T.AC AA.A. </pre>
<p>251</p> <pre> EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129bal-Drak GCPS18-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus </pre>	<p>300</p> <pre> CTATACC TGTCTGT.AA ATGTCCAATC AAAACCACTA CAGAACAAAG CTCCTATAAC TGT TTC. CATCAAAATG AGACTCA.G TGT TTC. CATCAAAATG AGACTACA.G TGT TTC. CATCAAAATG AGACTACA.G tttctgt.aa tgttccatc aaaatgacta tcgaacataa ttaatAtaac </pre>
<p>301</p> <pre> EMBH44836anti A TTGTTT ATACAAAGTT TCACT AAAT CTACAAACTT CCCCCGTAAA GCP18-5CP418L-Sams A TTGTTT ATACAAAGTT .CACT AAAT CTACAAACTT TCCCCGTAAA GCP18-2CP418L-Wes A TTGTTT ATACAAAGTT TCACT AAAT CTACAAACTT TCCCCGTAAA GCP18-4CP418L-R2000 A TTGTTT ATACAAAGTT .CACT AAAT CTACAAACTT TCCCCGTAAA conse129bal-Drak A. TGTTC ATACAAAGTT TCACT AAAT CTACAAACTT TCCCCGTAAA GCPS18-129Sam-ba2 A AC.CAGTTC TTGCA TAGTT TCACTAAAT CTACAAACTT TC. GCP18-3129R211-ba2 A ACACAGTTC TTGCA TAGTT TCACT.AAAT CTACAAACTT TC. GCP18-10129R20-ba2 A CCCAGTTC TTGCA TAGTT TC.CT.AAAT CTTCAAACTT TC. Consensus </pre>	<p>350</p>

Figure 15 (b)

	351	400
EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129bal-Drak GCPS18-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus	TGAGCTTAAT ATCACCCAA. GATGTTCA ATCAGAT AAA GAGTAACGAC TGAGCTTAAT ATCACCCAAA GATGTTCA ATCAGAT AAA GAGTAACGAC TGAGCTTAAT ATCACCCAAA GATGTTCA ATCAGAT AAA GAGTAACGAC TGAGCTTAAT ATCACCCAAA GATGTTCA ATCAGAT AAA GAGTAACGAC [.....] AAT CTTATCTAAA G.TTATCAC ATCA CAT GAA GA..... [.....] AAT CTTATCTAAA G.TTATCAC ATCA CAT GAA GA..... [.....] AAT CTTATCTAAA G.TTATCAC ATCA CAT GAA GA.....	400
EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129bal-Drak GCPS18-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus	ATCGTTTG GATTAGAACAA AA ATCGTTTG GATTAGAACAA AA ATCGTTTG GATTAGAACAA AA ATCGTTTG GATTAGAACAA AA ATCGTTTG GATTAGAACAA AA [.....] .GAGC AA [.....] .GCC AA [.....] .GCC A.	401
EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129bal-Drak GCPS18-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus	431	480
EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129bal-Drak GCPS18-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus	CTGAAACTTA CGTAGAGTGA TTTGAGGAGT AGGCTCGTT CCAGCAGAGC CTGAAACTTA CGTAGAGTGA TTTGAGGAGT AGGCTCGTT CCAGCAGAGC CTGAAACTTA CGTAGAGTGA TTTGAGGAGT AGGCTCGTT CCAGCAGAGC CTGAAACTTA CGTAGAGTGA TTTGAGGAGT AGGCTCGTT CCAGCAGAGC CTGAAACTTA CGTAGAGTGA TTTGAGGAGT AGGCTCGTT CCAGCAGAGC GTAACCTTA CTAGAGTGA TGAGGAGT AGGCTCGTT CCAGCAGAGC GTAACCTTA CTAGAGTGA TGAGGAGT AGGCTCGTT CCAGCAGAGC GTAACCTTA CTAGAGTGA TGAGGAGT AGGCTCGTT CCAGCAGAGC .t.aa.ctta c.tagagtga t.tgaggagt aggctcggt ccagc.gagc	480
EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129bal-Drak GCPS18-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus	481	530
EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129bal-Drak GCPS18-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus	TAGCTCTCTC CTCCGCCTCA TGAAGCATCT GTTGCACCTG AGACAACCGT TAGCTCTCTC ctccgcctca tgaagcatct g.tgcacctg agacaacccgt	530
EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129bal-Drak GCPS18-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus	531	580
EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129bal-Drak GCPS18-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus	GACGAAACTT TCCGATCACC GCCACCAGAA TTGAGGCCG CGCATCGGA GACGAAACTT TCCGATCCCC GCC.CCAGAA TTGAGGCCG CGCATCGGA gacgaaactt tccgatcacc gccaccagaa ttgagcccg cgcatcgga	580
EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129bal-Drak GCPS18-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus	581	630
EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129bal-Drak GCPS18-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus	GGATCCGAAT CGGGAACTGG AGTGAACCCG AGCGATCCCG GGAGTCGAC GGATCCGAAT cgggaaactgg agtgaaccg.g agcgatcccg ggagtccgac	630

Figure 15 (c)

	631		690		
EMBH44836anti	GGAGCGATGG	GAAAAGAGAG	TGGCACGATT	TCGACGAAGA	GTGGAAGAGG
GCP18-5CP418L-Sams	GGAGCGATGG	GAAAAGAGAG	TGGCACGATT	TCGACGAAGA	GTGGAAGAGG
GCP18-2CP418L-Wes	GGAGCGATGG	GAAAAGAGAG	TGGCACGATT	TCGACGAAGA	GTGGAAGAGG
GCP18-4CP418L-R2000	GGAGCGATGG	GAAAAGAGAG	TGGCACGATT	TCGACGAAGA	GTGGAAGAGG
conse129bal-Drak	GGAGCGATGG	GAAAAGAGAG	TGGCACGATT	TCGACGAAGA	GTGGAAGAGG
GCPS18-129Sam-ba2	GGAGCGATGG	A AAAAGAGAG	TGGCACGATT	TCGACGAAGA	C AGGAAGAGG
GCP18-3129R211-ba2	GGAGCGATGG	A AAAAGAGAG	TGGCACGATT	TCGACGAAGA	C AGGAAGAGG
GCP18-10129R20-ba2	GGAGCGATGG	A AAAAGAGAG	TGGCACGATT	TCG.CGAAGA	C AGGAAGAGG
Consensus	ggagcg.tgg	.aaaagagag	tggcacgatt	tcgacgaaga	g.ggaagagg
	691		740		
EMBH44836anti	AGAGGGTGGT	GGATAAAACTC	GGCTATGATC	AAGTTCTCA	TCGTCCCTGAT
GCP18-5CP418L-Sams	AGAGGGTGGT	GGATAAAACTC	GGCTATGATC	AAGTTCTCA	TCGTCCCTGAT
GCP18-2CP418L-Wes	AGAGGGTGGT	GGATAAAACTC	GGCTATGATC	AAGTTCTCA	TCGTCCCTGAT
GCP18-4CP418L-R2000	AGAGGGTGGT	GGATAAAACTC	GGCTATGATC	AAGTTCTCA	TCGTCCCTGAT
conse129bal-Drak	AGAGGGTGGT	GGATAAAACTC	GGCTATGATC	AAGTTCTCA	TCGTCCCTGAT
GCPS18-129Sam-ba2	AGAGGGTGGT	GGATAAAACTC	GGCTATGATC	AAGTTCTCA	TCGTCCCTGAT
GCP18-3129R211-ba2	AGAGGGTGGT	GGATAAAACTC	GGCTATGATC	AAGTTCTCA	TCGTCCCTGAT
GCP18-10129R20-ba2	AGAGGGTGGT	GGATAAAACTC	GGCTATGATC	AAGTTCTCA	TCGTCCCTGAA
Consensus	agagggtggt	ggataaaactc	gcgtatgatc	aagttctca	tcgtccctga.
	741		pSG129antiU 790		800
EMBH44836anti	TGCCGCCATT	TTTTTTGTCA	GGGCGCTCTG	TGGCTTAGAA	<u>GTTCCTCGATG</u>
GCP18-5CP418L-Sams	TGCCGCCATT	TTTTTTGTCA	GGGCGCTCTG	TGGCTTAGAA	GTTCCTCGATG
GCP18-2CP418L-Wes	TGCCGCCATT	TTTTTTGTCA	GGGCGCTCTG	TGGCTTAGAA	GTTCCTCGATG
GCP18-4CP418L-R2000	TGCCGCCATT	TTTTTTGTCA	GGGCGCTCTG	TGGCTTAGAA	GTTCCTCGATG.
conse129bal-Drak	TGCCGCCATT	TTTTTTGTCA	GGGCGCTCTG	.GGCTTAGAA	GTTCCTCGA..
GCPS18-129Sam-ba2	TGCCGCCATT	CTTGTTTCAC.	.GGCGCTCTG	GGT.....
GCP18-3129R211-ba2	TGCCGCC..
GCP18-10129R20-ba2	TGCC..CAT.	CTTGAGCTC.	.GG.GCGCGG	GCTCACAA..
Consensus	tgccgcat.	tt.....c.	.gg.gc.c.g
	791				
EMBH44836anti	TCAATGAAC	A	GTGACACGAC	GAAATGC	
GCP18-5CP418L-Sams	TCAATGAAC	AGAAT...TC	CGGG...		
GCP18-2CP418L-Wes	CCAATGAACA	AGATTATTC	CGATG..		
GCP18-4CP418L-R2000		
conse129bal-Drak		

Figure 16

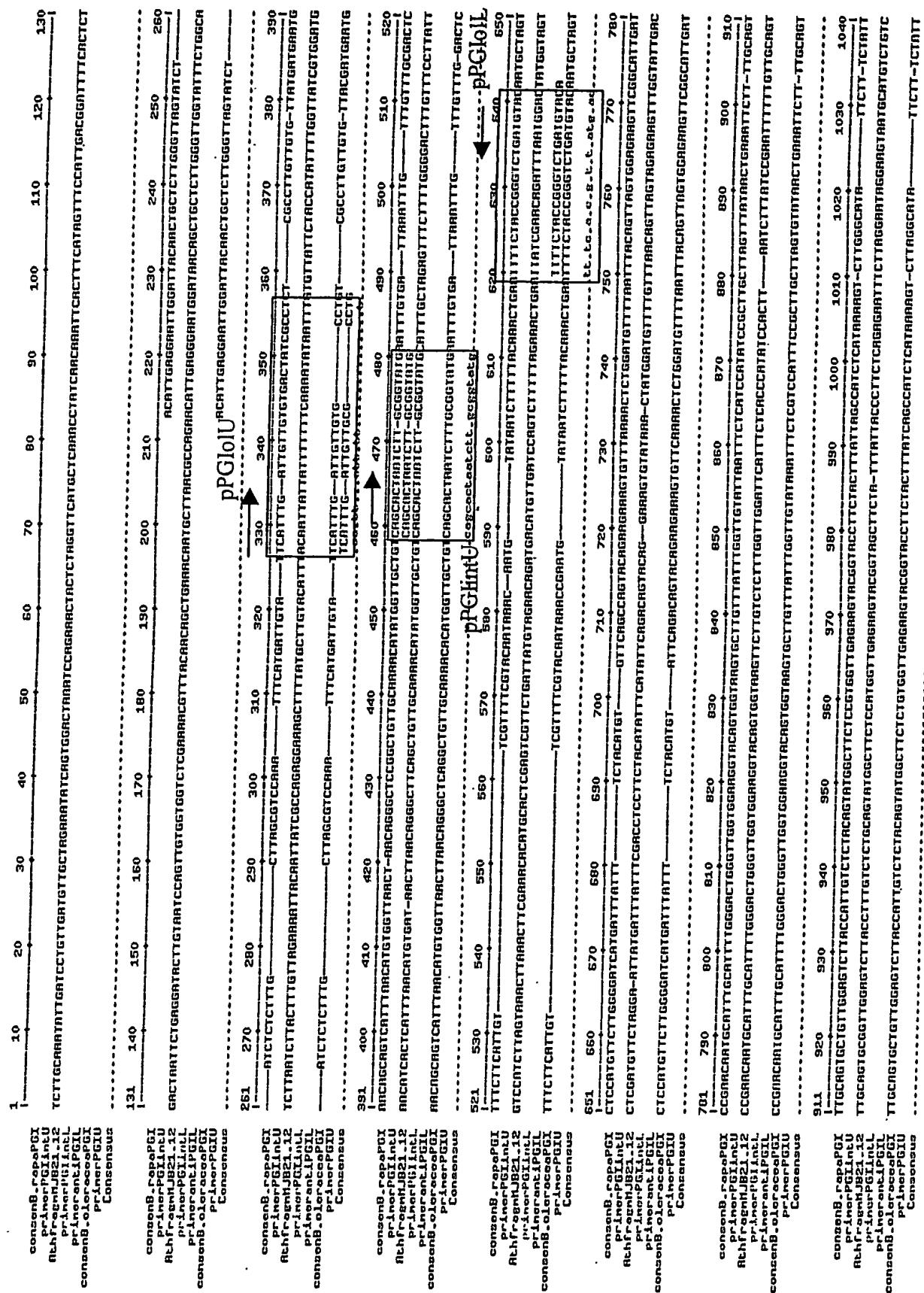


Figure 16 BIS

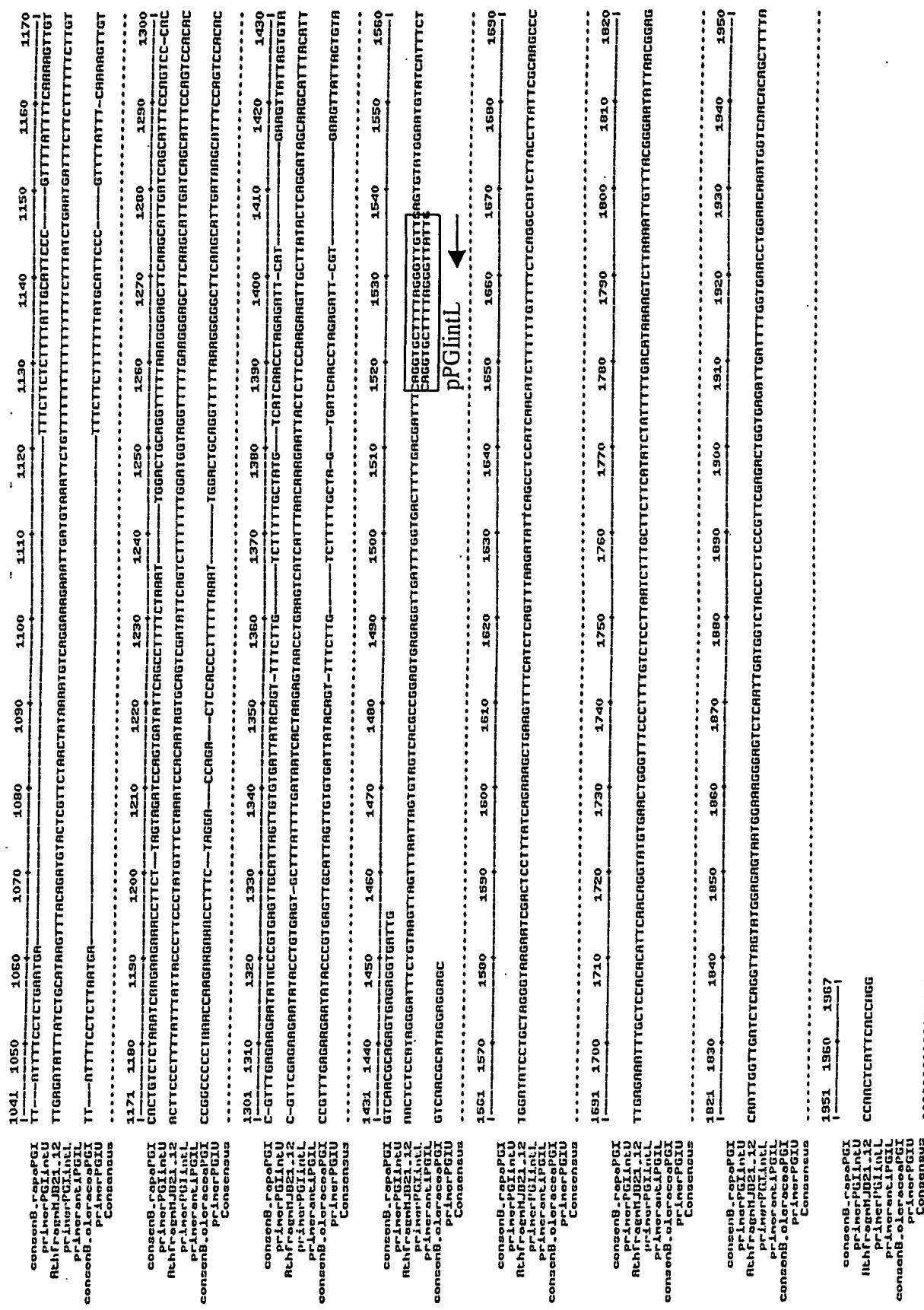


Figure 17

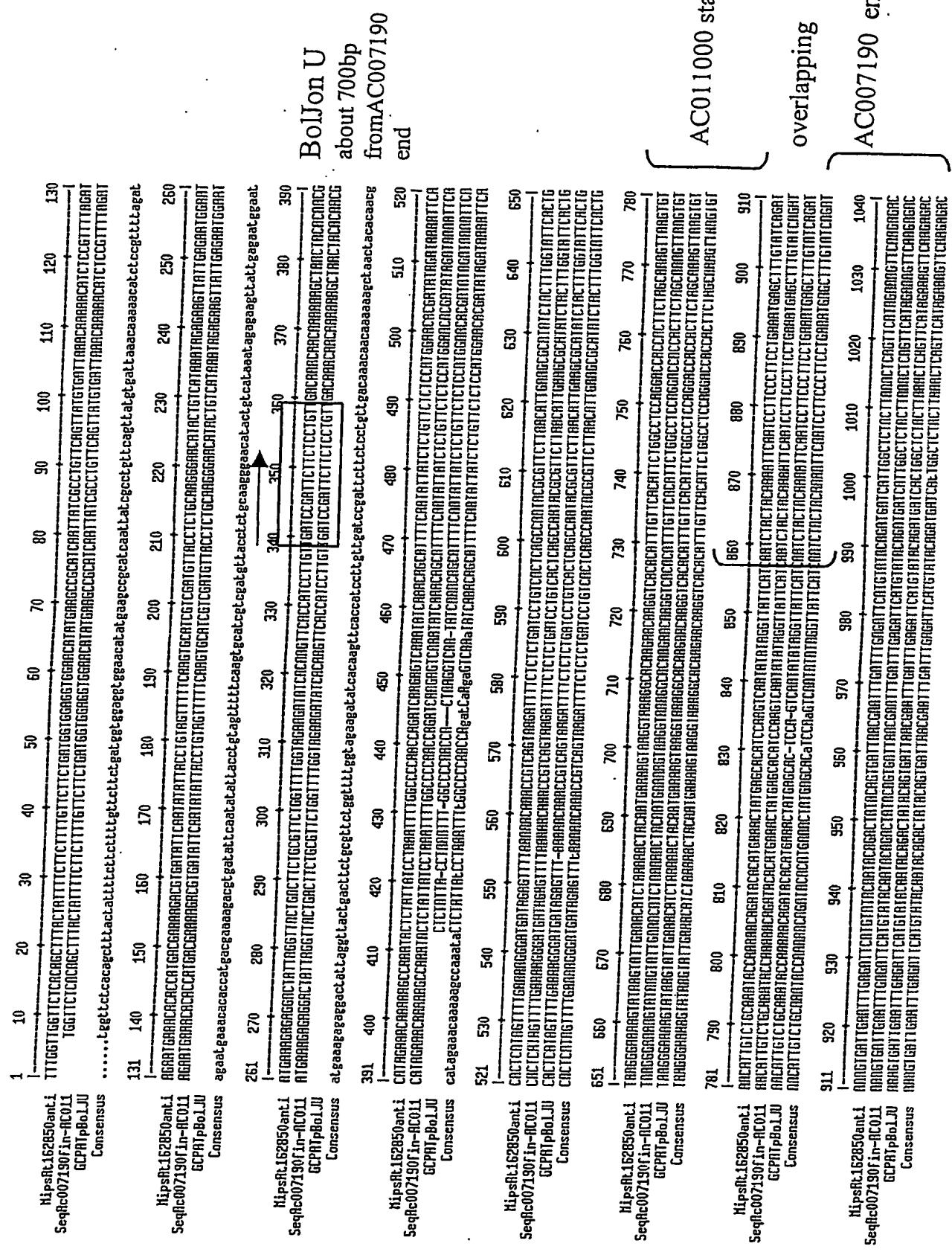


Figure 17 BIS

